

Replacement Table I

Sirna/ RPI#	Aliases	Sequence	SEQ ID#
25227	Sirna/RPI 21550 EGFR 3830L23 AS as siNA Str 1 (sense)	B UAACCUUGUACUGGUGCCUCC B	1
25228	Sirna/RPI 21550 EGFR 3830L23 AS as siNA Str 2 (antisense)	B GGAGGCACCAGUACGAGGUUA B	2
25229	Sirna/RPI 21549 EGFR as siNA Str 2 (antisense)	B AAACUCCAAGAUCGCCCAAUCA B	3
25230	Sirna/RPI 21549 EGFR 3 as siNA Str 1 (sense)	B UGAUUGGGGAUCUUGGAGUUU B	4
25231	Sirna/RPI 21547EGFR as siNA Str 2 (antisense)	B GUUGGAGUCUGUAGGACUUGG B	5
25232	Sirna/RPI 21547EGFR as siNA Str 1 (sense)	B CCAAGUCCUACAGACUCCAAC B	6
25233	Sirna/RPI 21545 EGFR as siNA Str 2 (antisense)	B GCAAAAACCCUGUGAUUUUCCU B	7
25234	Sirna/RPI 21545 EGFR as siNA Str 1 (sense)	B AGGAAAUACACAGGGUUUUUUGC B	8
25235	Sirna/RPI 21543 EGFR as siNA Str 2 (antisense)	B UUGGUCAGUUUCUGGCAGUUC B	9
25236	Sirna/RPI 21543 EGFR as siNA Str 1 (sense)	B GAACUGCCAGAAACUGACCAA B	10
25237	HCV IRES Loop IIb (Heptazyme site) as siNA str1 (sense)	B GGUCCUUUCUUGGAUCAACCC B	11
25238	HCV IRES Loop IIb (Heptazyme site) as siNA str2 (antisense)	B GGGUUGAUCCCAAGAAAGGACC B	12
25239	HBV (HepBzyme site) as siNA str1(sense) HBV (HepBzyme site) as siNA str2 (antisense)	B UGGACUUCUCUCAUUUUUCUA B	13
25240	HBV18371 site as siNA str1(sense)	B UAGAAAAUUAGAGAGAUCCA B	14
25241	HBV18371 site as siNA str2 (antisense)	B UUUUUCACCCUCUGCCUAAUCA B	15
25242	HBV18371 site as siNA str1(sense)	B UGAUUAGGCAGAGGUGAAAAA B	16
25243	HBV16372-18373 site as siNA str1(sense) HBV16372-18373 site as siNA str 2 (antisense)	B CAAGCCUCCAAGCUGUGCCUU B	17
25244	Sirna/RPI 17763 Her2Neu AS as siNA Str	B AAGGCACAGCUUGGAGGCUUG B	18
25245		B UCCAUGGUGCUCACUGCGGCU B	19

SiRNA/ RPI#	Aliases	Sequence	SEQ ID#
	2 (antisense)		
25246	SiRNA/RPI 17763 Her2Neu AS as siNA Str 1 (sense)	B AGCCGCAGUGAGCACCACCAUGGA B	20
25247	SiRNA/RPI 17763 Her2Neu AS as siNA Str 1 (sense) Inverted control	B AGGUACCCACGAGUGACGCCGA B	21
25248	SiRNA/RPI 17763 Her2Neu AS as siNA Str 1 (sense) Inverted control complement	B UCGGCGUCACUCUGUGGUACCU B	22
25249	SiRNA/RPI 21550 EGFR 3830L23 AS as siNA Str 1 (sense) Inverted Control	B CCUCCGUGGUGCAUGCUCCAAU B	23
25250	SiRNA/RPI 21550 EGFR 3830L23 AS as siNA Str 1 (sense) Inverted Control Complement	B AUUGGAGCAUGACCACGAGG B	24
25251	HCV IRES Loop IIb (Heptazyme site) as siNA str1 (sense) Inverted Control	B CCCAACUAGGUUCUUCUCCUGG B	25
25252	HCV IRES Loop IIb (Heptazyme site) as siNA str1 (sense) Inverted Control Complement	B CCAGGAAAGAACCUAGUUGGG B	26
25804	SiRNA/RPI 21550 EGFR 3830L23 AS as siNA Str 1 (sense) +2U overhang	UAACCUUGUACUGGUGCCUCCUU	27
25805	SiRNA/RPI 21550 EGFR 3830L23 AS as siNA Str 2 (antisense) +2U overhang	GGAGGCACCAGUACGAGGUUAUU	28
25806	SiRNA/RPI 21549 EGFR as siNA Str 2 (antisense)+ 2U overhang	AAACUCCAAGAUCUCCCAUAUU	29
25824	SiRNA/RPI 21550 EGFR 3830L23 AS as siNA Str 1 (sense) +2U overhang	BUAACCUUGUACUGGUGCCUCCUUB	30
25825	SiRNA/RPI 21550 EGFR 3830L23 AS as siNA Str 2 (antisense) +2U overhang	BGGAGGCACCAGUACGAGGUUAUUB	31
25826	SiRNA/RPI 21549 EGFR as siNA Str 2 (antisense)+ 2U overhang	BAAACUCCAAGAUCUCCCAUAUUB	32
25807	SiRNA/RPI 21549 EGFR 3 as siNA Str 1 (sense)+2U overhang	UGAUUGGGGAUCUUGGAGUUUUU	33
25808	SiRNA/RPI 21547EGFR as siNA Str 2 (antisense) +2U overhang	GUUGGAGUCUGUAGGACUUGGUU	34
25809	SiRNA/RPI 21547EGFR as siNA Str 1 (sense) + 2U overhang	CCAAGUCCUACAGACUCCAAUU	35
25827	SiRNA/RPI 21549 EGFR 3 as siNA Str 1 (sense)+2U overhang	BUGAUUGGGGAUCUUGGAGUUUUUB	36
25828	SiRNA/RPI 21547EGFR as siNA Str 2	BGUUGGAGUCUGUAGGACUUGGUUB	37

Sirna/ RPI#	Aliases	Sequence	SEQ ID#
	(antisense) +2U overhang		
25829	Sirna/RPI 21547 EGFR as siNA Str 1 (sense) + 2U overhang	BCCAAGUCCUACAGACUCCAACUUB	38
25810	Sirna/RPI 21545 EGFR as siNA Str 2 (antisense)+2U overhang	GCAAAAACCCUGUGAUUUUCCUUU	39
25811	Sirna/RPI 21545 EGFR as siNA Str 1 (sense)+2U overhang	AGGAAAUACACAGGGUUUUUGCUU	40
25812	Sirna/RPI 21543 EGFR as siNA Str 2 (antisense)+2U overhang	UUGGUCAGUUUCUGGCAGUUCUU	41
25830	Sirna/RPI 21545 EGFR as siNA Str 2 (antisense)+2U overhang	BGCAAAAACCCUGUGAUUUUCCUUUB	42
25831	Sirna/RPI 21545 EGFR as siNA Str 1 (sense)+2U overhang	BAGGAAAUACACAGGGUUUUUGCUUB	43
25832	Sirna/RPI 21543 EGFR as siNA Str 2 (antisense)+2U overhang	BUUGGUCAGUUUCUGGCAGUUCUUB	44
25813	Sirna/RPI 21543 EGFR as siNA Str 1 (sense)+2U overhang	GAACUGCCAGAAACUGACCAAUU	45
25814	HCV IRES Loop IIb (Heptazyme site) as siNA str1 (sense)+2U overhang	GGUCCUUUCUUGGAUCAACCCUU	46
25815	HCV IRES Loop IIb (Heptazyme site) as siNA str2 (antisense) +2U overhang	GGGUUGAUCCAAGAAAGGACCCUU	47
25833	Sirna/RPI 21543 EGFR as siNA Str 1 (sense)+2U overhang	BGAACUGCCAGAAACUGACCAAUUB	48
25834	HCV IRES Loop IIb (Heptazyme site) as siNA str1 (sense)+2U overhang	BGGUCCUUUCUUGGAUCAACCCUUB	49
25835	HCV IRES Loop IIb (Heptazyme site) as siNA str2 (antisense) +2U overhang	BGGGUUGAUCCAAGAAAGGACCCUUB	50
25816	HBV (HepBzyme site) as siNA str1 (sense)+2U overhang	UGGACUUUCUCUCAAUUUUUCUAUU	51
25817	HBV (HepBzyme site) as siNA str2 (antisense)+2U overhang	UAGAAAAUUGAGAGAGAAUGUCCAUU	52
25818	HBV18371 site as siNA str1(sense)+2U overhang	UUUUUCACCCUCUGCCUAAAUCAUU	53
25836	HBV (HepBzyme site) as siNA str1 (sense)+2U overhang	BUGGACUUUCUCUCAAUUUUUCUAUUUB	54
25837	HBV (HepBzyme site) as siNA str2 (antisense)+2U overhang	BUAGAAAAUUGAGAGAGAAUGUCCAUUB	55
25838	HBV18371 site as siNA str1(sense)+2U	BUUUUUACCCUCUCUGCCUAAAUCAUUB	56

Sirna/ RPI#	Aliases	Sequence	SEQ ID#
	overhang		
25819	HBV18371 site as siNA str2 (antisense)+2U overhang	UGAUUAGGCAGAGGUGAAAAUU	57
25820	HBV16372-18373 site as siNA str1 (sense)+2U overhang	CAAGCCUCCAAGCUGUGCCUUUU	58
25821	HBV16372-18373 site as siNA str 2 (antisense)+2U overhang	AAGGCACAGCUUGGAGGCUUGUU	59
25839	HBV18371 site as siNA str2 (antisense)+2U overhang	BUGAUUAGGCAGAGGUGAAAAUUB	60
25840	HBV16372-18373 site as siNA str1 (sense)+2U overhang	BCAAGCCUCCAAGCUGUGCCUUUUB	61
25841	HBV16372-18373 site as siNA str 2 (antisense)+2U overhang	BAAGGCACAGCUUGGAGGCUUGUUB	62
25822	Sirna/RPI 17763 Her2Neu AS as siNA Str 2 (antisense)+2U overhang	UCCAUGGUGCUCACUCGCGGCUUU	63
25823	Sirna/RPI 17763 Her2Neu AS as siNA Str 1 (sense)+2U overhang	AGCCGCAGUGAGCACCACCAUGGAUU	64
25842	Sirna/RPI 17763 Her2Neu AS as siNA Str 2 (antisense)+2U overhang	BUCCAUGGUGCUCACUCGCGGCUUUB	65
25843	Sirna/RPI 17763 Her2Neu AS as siNA Str 1 (sense)+2U overhang	BAGCCGCAGUGAGCACCACCAUGGAUUB	66
27649	Sirna/RPI GL2 Str1 (sense)	CGUACGCGGGAUAUCUUCGA TT	67
27650	Sirna/RPI GL2 Str2 (antisense)	UCGAAGUAUUCGCGGUACG TT	68
27651	Sirna/RPI Inverted GL2 Str1 (sense)	AGCUUCAUAAAGGCGCAUGC TT	69
27652	Sirna/RPI Inverted GL2 Str2 (antisense)	GCAUGCGCCUUUAUGAAGCU TT	70
27653	Sirna/RPI GL2 Str1 (sense) all ribo P=S	C <sub>5</sub> G <sub>5</sub> U <sub>5</sub> A <sub>5</sub> C <sub>5</sub> G <sub>5</sub> C <sub>5</sub> G <sub>5</sub> A <sub>5</sub> U <sub>5</sub> A <sub>5</sub> C <sub>5</sub> U <sub>5</sub> C <sub>5</sub> G <sub>5</sub> A TT	71
27654	Sirna/RPI GL2 Str1 (sense) all ribo pyrimidines P=S	C <sub>5</sub> GU <sub>5</sub> AC <sub>5</sub> GC <sub>5</sub> GGAAU <sub>5</sub> AC <sub>5</sub> U <sub>5</sub> C <sub>5</sub> GA TT	72
27655	Sirna/RPI GL2 Str1 (sense) 14 5' P=S	C <sub>5</sub> G <sub>5</sub> U <sub>5</sub> A <sub>5</sub> C <sub>5</sub> G <sub>5</sub> C <sub>5</sub> G <sub>5</sub> A <sub>5</sub> U <sub>5</sub> A <sub>5</sub> C <sub>5</sub> UUCGA TT	73
27656	Sirna/RPI GL2 Str1 (sense) 10 5' P=S	C <sub>5</sub> G <sub>5</sub> U <sub>5</sub> A <sub>5</sub> C <sub>5</sub> G <sub>5</sub> C <sub>5</sub> G <sub>5</sub> A <sub>5</sub> AUACUUCGA TT	74
27657	Sirna/RPI GL2 Str1 (sense) 5 5' P=S	C <sub>5</sub> G <sub>5</sub> U <sub>5</sub> A <sub>5</sub> C <sub>5</sub> GCGGAUAUACUUCGA TT	75
27658	Sirna/RPI GL2 Str2 (antisense) all ribo P=S	U <sub>5</sub> C <sub>5</sub> G <sub>5</sub> A <sub>5</sub> G <sub>5</sub> U <sub>5</sub> A <sub>5</sub> U <sub>5</sub> C <sub>5</sub> G <sub>5</sub> C <sub>5</sub> G <sub>5</sub> U <sub>5</sub> A <sub>5</sub> C <sub>5</sub> G TT	76
27659	Sirna/RPI GL2 Str2 (antisense) all ribo pyrimidines P=S	U <sub>5</sub> C <sub>5</sub> GAAGU <sub>5</sub> AU <sub>5</sub> C <sub>5</sub> C <sub>5</sub> GC <sub>5</sub> GU <sub>5</sub> AC <sub>5</sub> G TT	77
27660	Sirna/RPI GL2 Str2 (antisense) 5' 14 P=S	U <sub>5</sub> C <sub>5</sub> G <sub>5</sub> A <sub>5</sub> GU <sub>5</sub> A <sub>5</sub> U <sub>5</sub> C <sub>5</sub> C <sub>5</sub> G <sub>5</sub> C <sub>5</sub> GUACG TT	78

Sirna/ RPI#	Aliases	Sequence	SEQ ID#
27661	Sirna/RPI GL2 Str2 (antisense) 5' 10 P=S	U <sub>5</sub> C <sub>5</sub> G <sub>5</sub> A <sub>5</sub> A <sub>5</sub> G <sub>5</sub> U <sub>5</sub> A <sub>5</sub> U <sub>5</sub> U <sub>5</sub> CCGCGUACG TT	79
27662	Sirna/RPI GL2 Str2 (antisense) 5' 5 P=S	U <sub>5</sub> C <sub>5</sub> G <sub>5</sub> A <sub>5</sub> A <sub>5</sub> GUAUCCGCGUACG TT	80
28010	Sirna/RPI GL2 Str1 (sense) 5'ligation fragment	CGUACG	81
28011	Sirna/RPI GL2 Str1 (sense) 3' ligation fragment	CGGAUACUUCGATT	82
28012	Sirna/RPI GL2 Str2 (antisense) 5' ligation fragment	UCGAAGUA	83
28013	Sirna/RPI GL2 Str2 (antisense) 3'ligation fragment	UUCCGCGUACGTT	84
28254	Sirna/RPI GL2 Str1 (sense) all pyrimidines + TT = PS	C <sub>5</sub> GU <sub>5</sub> AC <sub>5</sub> GC <sub>5</sub> GGAU <sub>5</sub> AC <sub>5</sub> U <sub>5</sub> C <sub>5</sub> GAT <sub>5</sub> T	85
28255	Sirna/RPI GL2 Str2 (antisense), + TT = PS	UCGAAGUAUCCGCGUACGT <sub>5</sub> T	86
28256	Sirna/RPI GL2 Str2 (antisense), all pyrimidines+ TT = PS	U <sub>5</sub> C <sub>5</sub> GAAGU <sub>5</sub> AU <sub>5</sub> C <sub>5</sub> C <sub>5</sub> GC <sub>5</sub> GU <sub>5</sub> AC <sub>5</sub> GT <sub>5</sub> T	87
28262	Her2.1.sense Str1 (sense)	UGGGGUCGUCAAAGACGUUTT	88
28263	Her2.1.antisense Str2 (antisense)	AACGUCUUUGACGACCCCAT	89
28264	Her2.1.sense Str1 (sense) inverted	UUGCAGAAACUGCUGGGGUTT	90
28265	Her2.1.antisense Str2 (antisense) inverted	ACCCAGCAGUUUCUGCAATT	91
28266	Her2.2.sense Str1 (sense)	GGUGCUUGGAUCUGGGCGUTT	92
28267	Her2.2.antisense Str2 (antisense)	AGCGCCAGAUCCAAGCACCTT	93
28268	Her2.2.sense Str1 (sense) inverted	UCGCGGUCUAGGUUCGUGGTT	94
28269	Her2.2.antisense Str2 (antisense) inverted	CCACGAACCUAGACCGCGATT	95
28270	Her2.3.sense Str1 (sense)	GAUCUUUGGGAGCCUGGCATT	96
28271	Her2.3.antisense Str2 (antisense)	UGCCAGGCUCCCAAAGAUCTT	97
28272	Her2.3.sense Str1 (sense) inverted	ACGGUCCGAGGGUUUCUAGTT	98
28273	Her2.3.antisense Str2 (antisense) inverted	CUAGAAACCCUCGCGACCGUTT	99
28274	Sirna/RPI Inverted GL2 Str1 (sense) all ribo pyrimidines P=S	AGC <sub>5</sub> U <sub>5</sub> C <sub>5</sub> AU <sub>5</sub> AAGGC <sub>5</sub> GC <sub>5</sub> AU <sub>5</sub> GC TT	100
28275	Sirna/RPI Inverted GL2 Str1 (sense) 5' P=S	A <sub>5</sub> G <sub>5</sub> C <sub>5</sub> U <sub>5</sub> CAUAAGGCGCAUGC TT	101
28276	Sirna/RPI Inverted GL2 Str2 (antisense) all ribo pyrimidines P=S	GC <sub>5</sub> AU <sub>5</sub> GC <sub>5</sub> GC <sub>5</sub> C <sub>5</sub> U <sub>5</sub> AU <sub>5</sub> GAAGC <sub>5</sub> U TT	102
28277	Sirna/RPI Inverted GL2 Str2 (antisense) 5' 5' P=S	G <sub>5</sub> C <sub>5</sub> A <sub>5</sub> U <sub>5</sub> G <sub>5</sub> CGCCUUAUGAAGCU TT	103

Simla/ RPI#	Aliases	Sequence	SEQ ID#
28278	Simla/RPI Inverted GL2 Str2 (antisense) all ribo P=S	G <sub>5</sub> C <sub>5</sub> A <sub>5</sub> U <sub>5</sub> G <sub>5</sub> C <sub>5</sub> C <sub>5</sub> C <sub>5</sub> U <sub>5</sub> A <sub>5</sub> U <sub>5</sub> G <sub>5</sub> A <sub>5</sub> G <sub>5</sub> C <sub>5</sub> U TT	104
28279	Simla/RPI Inverted GL2 Str2 (antisense) 14 5' P=S	G <sub>5</sub> C <sub>5</sub> A <sub>5</sub> U <sub>5</sub> G <sub>5</sub> C <sub>5</sub> C <sub>5</sub> C <sub>5</sub> U <sub>5</sub> A <sub>5</sub> U <sub>5</sub> G <sub>5</sub> AAGCU TT	105
28280	Simla/RPI Inverted GL2 Str2 (antisense) 10 5' P=S	G <sub>5</sub> C <sub>5</sub> A <sub>5</sub> U <sub>5</sub> G <sub>5</sub> C <sub>5</sub> C <sub>5</sub> C <sub>5</sub> U <sub>5</sub> UAUGAAGCU TT	106
28383	hRelA.1.sense Str1 (sense)	CAGCACAGACCCAGCUGGTT	107
28384	hRelA.1.antisense Str2 (antisense)	CACAGCUGGGUCUGUGCUGTT	108
28385	hRelA.1.sense Str1 (sense) inverted	GUGUCGACCCAGACACGACTT	109
28386	hRelA.1.antisense Str2 (antisense) inverted	GUCGUGUCUGGGUCGACACTT	110
28387	hRelA.2.sense Str1 (sense)	GCAGGCUGGAGGUAAGGCCTT	111
28388	hRelA.2.antisense Str2 (antisense)	GGCCUJACCUCAGGCCUGCTT	112
28389	hRelA.2.sense Str1 (sense) inverted	CCGAAUGGAGGUCGGACGTT	113
28390	hRelA.2.antisense Str2 (antisense) inverted	CGUCCGACCUCCAUUCCGGTT	114
28391	h/mRelA.3.sense Str1 (sense)	GACUUCUCCUCCAUUGCGGTT	115
28392	h/mRelA.3.antisense Str2 (antisense)	CCGAAUGGAGGAGAAAGUCTT	116
28393	h/mRelA.3.sense Str1 (sense) inverted	GGCGUJACCUCUCCUUCAGTT	117
28394	h/mRelA.3.antisense Str2 (antisense) inverted	CUGAAGAGGAGGUAACGCCTT	118
28395	h/mRelA.4.sense Str1 (sense)	CACUGCCGAGGUCAGAAUCTT	119
28396	h/mRelA.4.antisense Str2 (antisense)	GAUCUUGAGGUCGGCAGUGTT	120
28397	h/mRelA.4.sense Str1 (sense) inverted	CUAGAACUCGAGCCGUCACTT	121
28398	h/mRelA.4.antisense Str2 (antisense) inverted	GUGACGGCUCGAGUUCUAGTT	122
28399	hIKKg.1.sense Str1 (sense)	GGAGUJCCUCUCAUGUGCAAAGTT	123
28400	hIKKg.1.antisense Str2 (antisense)	CUUGCACAUAGAGGAACUCCTT	124
28401	hIKKg.1.sense Str1 (sense) inverted	GAACGUGUACUCCUUGAGGTT	125
28402	hIKKg.1.antisense Str2 (antisense) inverted	CCUCAAGGAGUACACGUUUCTT	126
28403	hIKKg.2.sense Str1 (sense)	UCAAGAGCUCGAGAUAGCCTT	127
28404	hIKKg.2.antisense Str2 (antisense)	GGCAUCUCGGAGCUCUUGATT	128
28405	hIKKg.2.sense Str1 (sense) inverted	CCGUAGAGCCUCGAGAACUTT	129
28406	hIKKg.2.antisense Str2 (antisense) inverted	AGUUCUCGAGGCUUACGGTT	130
28407	h/mIKKg.sense Str1 (sense)	GCAGAUGGCUGAGGACAAAGTT	131
28408	h/mIKKg.3.antisense Str2 (antisense)	CUUGUCCUCAGCCAUUCUGCTT	132

Sirna/ RPI#	Aliases	Sequence	SEQ ID#
28409	h/miKKG.3.sense Str1 (sense) inverted	GAACAGGAGUCGGUAGACGTT	133
28410	h/miKKG.3.antisense Str2 (antisense) inverted	CGUCUACCGACUCCUGUUCTT	134
28447	Sirna/RPI construct as hairpin +GAAA+AU blunt	AACGUACGCGGAAUACUUCGAUUAAGAAUAAUUCGCGGUACGUU	135
28448	Sirna/RPI construct as hairpin +GAAA+AU 3' overhang	CGUACGCGGAAUACUUCGAUUAAGAAUAAUUCGCGGUACGUU	136
28449	Sirna/RPI construct as hairpin +GAAA blunt	AACGUACGCGGAAUACUUCGAUUAAGAAUAAUUCGCGGUACGUU	137
28450	Sirna/RPI construct as hairpin +GAAA 3' overhang	CGUACGCGGAAUACUUCGAUUAAGAAUAAUUCGCGGUACGUU	138
28451	Sirna/RPI construct as hairpin +UUG 3' overhang	CGUACGCGGAAUACUUCGAUUAAGAAUAAUUCGCGGUACGUU	139
28452	Sirna/RPI construct as hairpin +UUG blunt	AACGUACGCGGAAUACUUCGAUUAAGAAUAAUUCGCGGUACGUU	140
28453	Sirna/RPI construct as hairpin +UUG+AU blunt	AACGUACGCGGAAUACUUCGAUUAAGAAUAAUUCGCGGUACGUU	141
28454	Sirna/RPI construct as hairpin +UUG 3' overhang	CGUACGCGGAAUACUUCGAUUAAGAAUAAUUCGCGGUACGUU	142
28415	HCV-Luc:325U21 TT siNA (sense)	CCCCGGGAGGUCUCGUAGATT	143
28416	HCV-Luc:162U21 TT siNA (sense)	CGGAACCGGUGAGUACACCTT	144
28417	HCV-Luc:324U21 TT siNA (sense)	GCCCCGGGAGGUCUCGUAGTT	145
28418	HCV-Luc:163U21 TT siNA (sense)	GGAACCGGUGAGUACACCGTT	146
28419	HCV-Luc:294U21 TT siNA (sense)	GUGGUACUGCCUGAUAGGGTT	147
28420	HCV-Luc:293U21 TT siNA (sense)	UGUGGUACUGCCUGAUAGGGTT	148
28421	HCV-Luc:292U21 TT siNA (sense)	UUGUGGUACUGCCUGAUAGTT	149
28422	HCV-Luc:343L21 TT siNA (325C) (antisense)	UCUACGAGACCUCCCGGGGTT	150
28423	HCV-Luc:180L21 TT siNA (162C) (antisense)	GGUGUACUACCGGUUCCGTT	151
28424	HCV-Luc:342L21 TT siNA (324C) (antisense)	CUACGAGACCUCCCGGGGCTT	152
28425	HCV-Luc:181L21 TT siNA (163C) (antisense)	CGGUGUACUACCGGUUCCCTT	153
28426	HCV-Luc:312L21 TT siNA (294C) (antisense)	CCCUAUCAGGCAGUACCACTT	154
28427	HCV-Luc:311L21 TT siNA (293C) (antisense)	CCUAUCAGGCAGUACCACTT	155

Sirna/ RPI#	Aliases	Sequence	SEQ ID#
28428	HCV-Luc:310L21 TT siNA (292C) (antisense)	CUAUCAGGCAGUACCAAT	156
28429	HCV-Luc:325U21 TT siNA (sense) inv	TTAGAUGCUCUGGAGGCCCC	157
28430	HCV-Luc:162U21 TT siNA (sense) inv	TTCCACAUGAGUGGCCAAGGC	158
28431	HCV-Luc:324U21 TT siNA (sense) inv	TTGAUGCUCUGGAGGCCCCCG	159
28432	HCV-Luc:163U21 TT siNA (sense) inv	TTGCCACAUGAGUGGCCAAGG	160
28433	HCV-Luc:294U21 TT siNA (sense) inv	TTGGGAUAGUCCGUCAUUGGUG	161
28434	HCV-Luc:293U21 TT siNA (sense) inv	TTGGAUAGUCCGUCAUUGGUGU	162
28435	HCV-Luc:292U21 TT siNA (sense) inv	TTGAUAGUCCGUCAUUGGUGUU	163
28436	HCV-Luc:343L21 TT siNA (325C) (antisense) inv	TTGGGGCCCUCCAGAGCAUCU	164
28437	HCV-Luc:180L21 TT siNA (162C) (antisense) inv	TTGCCUUUGGCCACUCAUGUGG	165
28438	HCV-Luc:342L21 TT siNA (324C) (antisense) inv	TTGGGGCCCUCCAGAGCAUC	166
28439	HCV-Luc:181L21 TT siNA (163C) (antisense) inv	TTCCUUUGGCCACUCAUGUGGC	167
28440	HCV-Luc:312L21 TT siNA (294C) (antisense) inv	TTCACCAUGACGGACUAUCCC	168
28441	HCV-Luc:311L21 TT siNA (293C) (antisense) inv	TTACACCAUGACGGACUAUCC	169
28442	HCV-Luc:310L21 TT siNA (292C) (antisense) inv	TTAACACCAUGACGGACUAUC	170
28458	Sirna/RPI Inverted GL2 Str1 (sense) 5' 5' P=S + TsT	A <sub>5</sub> G <sub>5</sub> C <sub>5</sub> U <sub>5</sub> CAUAAAGCGCAUGC T <sub>5</sub> T	171
28459	Sirna/RPI Inverted GL2 Str2 (antisense) 5' 5' P=S + TsT	G <sub>5</sub> C <sub>5</sub> A <sub>5</sub> U <sub>5</sub> G <sub>5</sub> CGCCUUUAUGAAGCU T <sub>5</sub> T	172
28460	Sirna/RPI GL2 Str1 (sense) 5' 5' P=S + TsT	C <sub>5</sub> G <sub>5</sub> U <sub>5</sub> A <sub>5</sub> C <sub>5</sub> GCGGAUACUUCGA T <sub>5</sub> T	173
28461	TsT	U <sub>5</sub> C <sub>5</sub> G <sub>5</sub> A <sub>5</sub> GUAUUCGCGUACG T <sub>5</sub> T	174
28511	Sirna/RPI GL2 Str2 (antisense) + Sirna/RPI GL2 Str1 (sense) (tandem synth. w/ idB on 3' of Str 1)	CGUACGGGGAUACUUCGATTBUCGAAGUAUCCGCGUACG TT	175
29543	HBV:248U21 siNA pos (sense)	GUCUAGACUCUGGUGGACTT	176
29544	HBV:414U21 siNA pos (sense)	CCUGCUGCUAUGCCUCAUCTT	177
29545	HBV:1867U21 siNA pos (sense)	CAAGCCUCCAAGCUGUGCCCTT	178



Sirna/ RPI#	Aliases	Sequence	SEQ ID#
29546	HBV:1877U21 siNA pos (sense)	AGCUGUGCCUUGGUGGCUUTT	179
29547	HBV:228L21 siNA neg (248C) (antisense)	GUCCACCACGAGUCUAGACTT	180
29548	HBV:394L21 siNA neg (414C) (antisense)	GAUGAGGCAUAGCAGCAGGTT	181
29549	HBV:1847L21 siNA neg (1867C) (antisense)	GGCACAGCUUGGAGGGCUUGTT	182
29550	HBV:1857L21 siNA neg (1877C) (antisense)	AGCCACCCAAAGGCACAGCUTT	183
29551	HBV:248U21 siNA pos (sense) inv	CAGGUGGUGCUCAGAUUCUGTT	184
29552	HBV:414U21 siNA pos (sense) inv	CUACUCCGUUUCGUGUCCCTT	185
29553	HBV:1867U21 siNA pos (sense) inv	CCGUGUCGAACCUCCGAACCTT	186
29554	HBV:1877U21 siNA pos (sense) inv	UCGGUGGGUUCGUGUCGATT	187
29555	HBV:228L21 siNA neg (248C) (antisense) inv	CAGAUCUGAGCACCACCUGTT	188
29556	HBV:394L21 siNA neg (414C) (antisense) inv	GGACGACGUAUCGGAGUAGTT	189
29557	HBV:1847L21 siNA neg (1867C) (antisense) inv	GUUCGGAGGUUCGACACCGTT	190
29558	HBV:1857L21 siNA neg (1877C) (antisense) inv	UCGACACGGAAACCCACCGATT	191
29573	HCV-Luc:162U21 siNA (sense)	CGGAACCCGGUGAGUACACCCGG	192
29574	HCV-Luc:163U21 siNA (sense)	GGAAACCCGGUGAGUACACCCGA	193
29575	HCV-Luc:292U21 siNA (sense)	UUGUGGUACUGCCUGAUAGGGG	194
29576	HCV-Luc:293U21 siNA (sense)	UGUGGUACUGCCUGAUAGGGU	195
29577	HCV-Luc:294U21 siNA (sense)	GUGGUACUGCCUGAUAGGGUG	196
29578	HCV-Luc:324U21 siNA (sense)	GCCCCGGGAGGUCUCGUAGAC	197
29579	HCV-Luc:325U21 siNA (sense)	CCCCGGGAGGUCUCGUAGACC	198
29580	HCV-Luc:182L21 siNA (162C) (antisense)	GGUGUACUCACCCGUUCCGCA	199
29581	HCV-Luc:183L21 siNA (163C) (antisense)	CGGUGUACUCACCCGUUCCCGC	200
29582	HCV-Luc:312L21 siNA (292C) (antisense)	CUAUCAGGCAGUACCAACAAG	201
29583	HCV-Luc:313L21 siNA (293C) (antisense)	CCUAUCAGGCAGUACCAACAAG	202
29584	HCV-Luc:314L21 siNA (294C) (antisense)	CCUAUCAGGCAGUACCAACA	203
29585	HCV-Luc:344L21 siNA (324C) (antisense)	CUACGAGACCUCCCGGGGCAC	204
29586	HCV-Luc:345L21 siNA (325C) (antisense)	UCUACGAGACCUCCCGGGGCA	205
29587	HCV-Luc:162U21 siNA (sense) rev	GGCCACAUGAGUGGCCCAAGGC	206

Sirna/ RPI#	Aliases	Sequence	SEQ ID#
29588	HCV-Luc:163U21 siNA (sense) rev	AGCCACAUGAGUGGCCAAGG	207
29589	HCV-Luc:292U21 siNA (sense) rev	GGGAUAGUCCGUCAGUGGUU	208
29590	HCV-Luc:293U21 siNA (sense) rev	UGGGAUAGUCCGUCAGUGGUU	209
29591	HCV-Luc:294U21 siNA (sense) rev	GUGGAUAGUCCGUCAGUGGUU	210
29592	HCV-Luc:324U21 siNA (sense) rev	CAGAUGCUCUGGAGGGCCCCCG	211
29593	HCV-Luc:325U21 siNA (sense) rev	CCAGAUGCUCUGGAGGGCCCCCG	212
29594	HCV-Luc:182L21 siNA (162C) (antisense) rev	ACGCCUUGGCCACUCUAUGUGG	213
29595	HCV-Luc:183L21 siNA (163C) (antisense) rev	CGCCUUGGCCACUCUAUGUGGC	214
29596	HCV-Luc:312L21 siNA (292C) (antisense) rev	GGAACACCAUGACGGACUAUC	215
29597	HCV-Luc:313L21 siNA (293C) (antisense) rev	GAACACCAUGACGGACUAUCC	216
29598	HCV-Luc:314L21 siNA (294C) (antisense) rev	AACACCAUGACGGACUAUCCC	217
29599	HCV-Luc:344L21 siNA (324C) (antisense) rev	CACGGGGCCUCCAGAGCAUC	218
29600	HCV-Luc:345L21 siNA (325C) (antisense) rev	ACGGGGCCUCCAGAGCAUCU	219
29601	Luc2:128U21 siNA (sense)	CAGAUGCACAUAUCGAGGUGA	220
29602	Luc3:128U21 siNA (sense)	CAGAUGCACAUAUCGAGGUGG	221
29603	Luc2/3:128U21 TT siNA (sense)	CAGAUGCACAUAUCGAGGUTT	222
29604	Luc2/3:148L21 siNA (128C) (antisense)	ACCUCGAUAUGUGCAUCUGUA	223
29605	Luc2/3:148L21 TT siNA (128C) (antisense)	ACCUCGAUAUGUGCAUCUGTT	224
29606	Luc2/3:166U21 siNA (sense)	UACUUCGAAAUGUCCGUUCGG	225
29607	Luc2/3:166U21 TT siNA (sense)	UACUUCGAAAUGUCCGUUCTT	226
29608	Luc2:186L21 siNA (166C) (antisense)	GAACGGACAUAUUCGAAAGUAUU	227
29609	Luc3:186L21 siNA (166C) (antisense)	GAACGGACAUAUUCGAAAGUAUU	228
29610	Luc2/3:186L21 TT siNA (166C) (antisense)	GAACGGACAUAUUCGAAAGUAUU	229
29611	Luc2/3:167U21 siNA (sense)	ACUUCGAAAUGUCCGUUCGGU	230
29612	Luc2/3:167U21 TT siNA (sense)	ACUUCGAAAUGUCCGUUCGTT	231
29613	Luc2:187L21 siNA (167C) (antisense)	CGAACGGACAUAUUCGAAAGUAUU	232
29614	Luc3:187L21 siNA (167C) (antisense)	CGAACGGACAUAUUCGAAAGUAUU	233

Sirna/ RPI#	Aliases	Sequence	SEQ ID#
29615	Luc2/3:187L21 TT siNA (167C) (antisense)	CGAACGGACAUUUCGAAGUTT	234
29616	Luc2/3:652U21 siNA (sense)	AGAUUCUCGCAUGCCAGAGAU	235
29617	Luc2/3:652U21 TT siNA (sense)	AGAUUCUCGCAUGCCAGAGTT	236
29618	Luc2:672L21 siNA (652C) (antisense)	CUCUGGCAUGCGAGAAUCUGA	237
29619	Luc3:672L21 siNA (652C) (antisense)	CUCUGGCAUGCGAGAAUCUCA	238
29620	Luc2/3:672L21 TT siNA (652C) (antisense)	CUCUGGCAUGCGAGAAUCUTT	239
29621	Luc2/3:653U21 siNA (sense)	GAUUCUCGCAUGCCAGAGAUC	240
29622	Luc2/3:653U21 TT siNA (sense)	GAUUCUCGCAUGCCAGAGATT	241
29623	Luc2:673L21 siNA (653C) (antisense)	UCUCUGGCAUGCGAGAAUCUG	242
29624	Luc3:673L21 siNA (653C) (antisense)	UCUCUGGCAUGCGAGAAUCUC	243
29625	Luc2/3:673L21 TT siNA (653C) (antisense)	UCUCUGGCAUGCGAGAAUCTT	244
29626	Luc2/3:880U21 siNA (sense)	UUCUUCGCCAAAAGCACUCUG	245
29627	Luc2/3:880U21 TT siNA (sense)	UUCUUCGCCAAAAGCACUCTT	246
29628	Luc2:900L21 siNA (880C) (antisense)	GAGUGCUUUUGGCGAAGAAUG	247
29629	Luc3:900L21 siNA (880C) (antisense)	GAGUGCUUUUGGCGAAGAAAGG	248
29630	Luc2/3:900L21 TT siNA (880C) (antisense)	GAGUGCUUUUGGCGAAGAAATT	249
29631	Luc2/3:1012U21 siNA (sense)	CAAGGAUAUGGGCUCACUGAG	250
29632	Luc2/3:1012U21 TT siNA (sense)	CAAGGAUAUGGGCUCACUGTT	251
29633	Luc2:1032L21 siNA (1012C) (antisense)	CAGUGAGCCCAUAUCCUUGUC	252
29634	Luc3:1032L21 siNA (1012C) (antisense)	CAGUGAGCCCAUAUCCUUGCC	253
29635	Luc2/3:1032L21 TT siNA (1012C) (antisense)	CAGUGAGCCCAUAUCCUUGTT	254
29636	Luc2:1139U21 siNA (sense)	AAACGCGUGGCGUUAAUCAGA	255
29637	Luc3:1139U21 siNA (sense)	AAACGCGUGGCGUUAAUCAA	256
29638	Luc2/3:1139U21 TT siNA (sense)	AAACGCGUGGCGUUAAUCATT	257
29639	Luc2/3:1159L21 siNA (1139C) (antisense)	UGAUUACGCCCGAGCGUUUUC	258
29640	Luc2/3:1159L21 TT siNA (1139C) (antisense)	UGAUUACGCCCGAGCGUUUTT	259
29641	Luc2:1283U21 siNA (sense)	AAGACGAACACUUCUUAUAG	260
29642	Luc3:1283U21 siNA (sense)	AAGACGAACACUUCUUAUCG	261
29643	Luc2/3:1283U21 TT siNA (sense)	AAGACGAACACUUCUUAUUTT	262
29644	Luc2/3:1303L21 siNA (1283C) (antisense)	AUGAAGAAAGUGUUCGUCUUCG	263
29645	Luc2/3:1303L21 TT siNA (1283C)	AUGAAGAAAGUGUUCGUCUUTT	264

Sirna/ RPI#	Aliases	Sequence	SEQ ID#
	(antisense)		
29646	Luc2:1487U21 siNA (sense)	AAGAGAUUCGUGGAUUACGUGG	265
29647	Luc3:1487U21 siNA (sense)	AAGAGAUUCGUGGAUUACGUCG	266
29648	Luc2/3:1487U21 TT siNA (sense)	AAGAGAUUCGUGGAUUACGUTT	267
29649	Luc2/3:1507L21 siNA (1487C) (antisense)	ACGUAAUCCACGAUCUCUUUU	268
29650	Luc2/3:1507L21 TT siNA (1487C) (antisense)	ACGUAAUCCACGAUCUCUUTT	269
29651	Luc2:1622U21 siNA (sense)	AGGCCAAGAAAGGGGGGAAAGU	270
29652	Luc3:1622U21 siNA (sense)	AGGCCAAGAAAGGGGGGAAAGA	271
29653	Luc2/3:1622U21 TT siNA (sense)	AGGCCAAGAAAGGGGGGAAATT	272
29654	Luc2/3:1642L21 siNA (1622C) (antisense)	UUUCGCCCCUUCUUGGCCUUU	273
29655	Luc2/3:1642L21 TT siNA (1622C) (antisense)	UUUCGCCCCUUCUUGGCCUTT	274
29656	Luc2:1623U21 siNA (sense)	GGCCAAGAAAGGGGGGAAAGUC	275
29657	Luc3:1623U21 siNA (sense)	GGCCAAGAAAGGGGGGAAAGAU	276
29658	Luc2/3:1623U21 TT siNA (sense)	GGCCAAGAAAGGGGGGAAAGTT	277
29659	Luc2/3:1643L21 siNA (1623C) (antisense)	CUUUCGCCCCUUCUUGGCCUU	278
29660	Luc2/3:1643L21 TT siNA (1623C) (antisense)	CUUUCGCCCCUUCUUGGCCCTT	279
29663	Sirna/RPI GL2 Str2 (antisense), all pyrimidines+ 5BrdUT = PS	U <sub>5</sub> C <sub>5</sub> GAAAU <sub>5</sub> AU <sub>5</sub> U <sub>5</sub> C <sub>5</sub> C <sub>5</sub> GC <sub>5</sub> GU <sub>5</sub> AC <sub>5</sub> GU <sub>5</sub> T	280
29664	Sirna/RPI GL2 Str1 (sense) all pyrimidines + 5-BrdUT = PS	C <sub>5</sub> GU <sub>5</sub> AC <sub>5</sub> GC <sub>5</sub> GGAAU <sub>5</sub> AC <sub>5</sub> U <sub>5</sub> U <sub>5</sub> C <sub>5</sub> GAU <sub>5</sub> T	281
29665	Sirna/RPI GL2 Str1 (sense) 5' 5' +5-BrdUT = P=S	C <sub>5</sub> G <sub>5</sub> U <sub>5</sub> A <sub>5</sub> C <sub>5</sub> GC <sub>5</sub> GGAAU <sub>5</sub> AC <sub>5</sub> U <sub>5</sub> U <sub>5</sub> C <sub>5</sub> GAU <sub>5</sub> T	282
29666	Sirna/RPI GL2 Str2 (antisense) 5' 5' +5BrdUT= P=S	U <sub>5</sub> C <sub>5</sub> G <sub>5</sub> A <sub>5</sub> A <sub>5</sub> GUAUUCGCGGUACG U <sub>5</sub> T	283
29667	Sirna/RPI GL2 Str1 (sense) all pyrimidines + TT = PS+3'invAba	C <sub>5</sub> GU <sub>5</sub> AC <sub>5</sub> GC <sub>5</sub> GGAAU <sub>5</sub> AC <sub>5</sub> U <sub>5</sub> U <sub>5</sub> C <sub>5</sub> GAT <sub>5</sub> TB	284
29668	Sirna/RPI GL2 Str1 (sense) all pyrimidines = PS+3' and 5' invAba	BC <sub>5</sub> GU <sub>5</sub> AC <sub>5</sub> GC <sub>5</sub> GGAAU <sub>5</sub> AC <sub>5</sub> U <sub>5</sub> U <sub>5</sub> C <sub>5</sub> GAT <sub>5</sub> TB	285
29669	Sirna/RPI GL2 Str1 (sense) all pyrimidines + TT = PS+ 5' invAba	BC <sub>5</sub> GU <sub>5</sub> AC <sub>5</sub> GC <sub>5</sub> GGAAU <sub>5</sub> AC <sub>5</sub> U <sub>5</sub> U <sub>5</sub> C <sub>5</sub> GAT <sub>5</sub> T	286
29670	Sirna/RPI GL2 Str2 (antisense), all pyrimidines +TT = PS + 3'inverted abasic	U <sub>5</sub> C <sub>5</sub> GAAGU <sub>5</sub> AU <sub>5</sub> U <sub>5</sub> C <sub>5</sub> C <sub>5</sub> GC <sub>5</sub> GU <sub>5</sub> AC <sub>5</sub> GT <sub>5</sub> TB	287
29671	Sirna/RPI GL2 Str2 (antisense), all	BU <sub>5</sub> C <sub>5</sub> GAAGU <sub>5</sub> AU <sub>5</sub> U <sub>5</sub> C <sub>5</sub> C <sub>5</sub> GC <sub>5</sub> GU <sub>5</sub> AC <sub>5</sub> GT <sub>5</sub> TB	288

Sirna/ RPI#	Aliases	Sequence	SEQ ID#
	pyrimidines +TT = PS + 3' and 5' inverted <i>abasic</i>		
29672	Sirna/RPI GL2 Str2 (antisense), all pyrimidines +TT = PS + 5' inverted <i>abasic</i>	BU <sub>5</sub> C <sub>5</sub> GAAGU <sub>5</sub> AU <sub>5</sub> C <sub>5</sub> C <sub>5</sub> GC <sub>5</sub> GU <sub>5</sub> AC <sub>5</sub> GT <sub>5</sub> T	289
29678	Sirna/RPI GL2 Str1 (sense) + Sirna/RPI GL2 Str2 (antisense) (tandem synth. w/ idB on 3' of Str 2)	UCGAAGUAUUCCGCGUACG TTBCGUACGCGGAUACUUCGATT	290
29681	Sirna/RPI GL2 Str1 (sense) 5' ligation fragment 5'-P=S	C <sub>5</sub> G <sub>5</sub> U <sub>5</sub> A <sub>5</sub> C <sub>5</sub> G	291
29682	Sirna/RPI GL2 Str1 (sense) 3' ligation fragment 5'-P=S	CGGAUACUUCGAT <sub>5</sub> T	292
29683	Sirna/RPI GL2 Str2 (antisense) 5' ligation fragment 5'-P=S	U <sub>5</sub> C <sub>5</sub> G <sub>5</sub> A <sub>5</sub> A <sub>5</sub> GUA	293
29684	Sirna/RPI GL2 Str2 (antisense) 3' ligation fragment 5'-P=S	UUCCGCGUACGT <sub>5</sub> T	294
29685	Sirna/RPI GL2 Str2 (antisense) 5' ligation fragment all-P=S	U <sub>5</sub> C <sub>5</sub> G <sub>5</sub> A <sub>5</sub> A <sub>5</sub> G <sub>5</sub> U <sub>5</sub> A	295
29686	Sirna/RPI GL2 Str2 (antisense) 3' ligation fragment all-P=S	U <sub>5</sub> U <sub>5</sub> C <sub>5</sub> C <sub>5</sub> G <sub>5</sub> C <sub>5</sub> G <sub>5</sub> U <sub>5</sub> A <sub>5</sub> C <sub>5</sub> G <sub>5</sub> T <sub>5</sub> T	296
29694	FLT1:349U21 siNA stab1 (sense)	C <sub>5</sub> U <sub>5</sub> G <sub>5</sub> A <sub>5</sub> G <sub>5</sub> UUUAAAAGGCACCT <sub>5</sub> T	297
29695	FLT1:2340U21 siNA stab1 (sense)	C <sub>5</sub> A <sub>5</sub> A <sub>5</sub> C <sub>5</sub> C <sub>5</sub> ACAAAUAACAAT <sub>5</sub> T	298
29696	FLT1:3912U21 siNA stab1 (sense)	C <sub>5</sub> C <sub>5</sub> U <sub>5</sub> G <sub>5</sub> G <sub>5</sub> AAAGAAUCAAACCT <sub>5</sub> T	299
29697	FLT1:2949U21 siNA stab1 (sense)	G <sub>5</sub> C <sub>5</sub> A <sub>5</sub> A <sub>5</sub> G <sub>5</sub> GAGGGCCUCUGAUGT <sub>5</sub> T	300
29698	FLT1:369L21 siNA (349C) stab1 (antisense)	G <sub>5</sub> G <sub>5</sub> G <sub>5</sub> U <sub>5</sub> G <sub>5</sub> CCUUUUAAACUCAGT <sub>5</sub> T	301
29699	FLT1:2360L21 siNA (2340C) stab1 (antisense)	U <sub>5</sub> U <sub>5</sub> G <sub>5</sub> U <sub>5</sub> U <sub>5</sub> GUUUUUUGUGGUUGT <sub>5</sub> T	302
29700	FLT1:3932L21 siNA (3912C) stab1 (antisense)	G <sub>5</sub> G <sub>5</sub> U <sub>5</sub> U <sub>5</sub> U <sub>5</sub> UGAUUCUUUCCAGGT <sub>5</sub> T	303
29701	FLT1:2969L21 siNA (2949C) stab1 (antisense)	C <sub>5</sub> A <sub>5</sub> U <sub>5</sub> C <sub>5</sub> A <sub>5</sub> GAGGCCCUCCUUGCT <sub>5</sub> T	304
29706	FLT1:369L21 siNA (349C) (antisense) stab2	G <sub>5</sub> G <sub>5</sub> G <sub>5</sub> U <sub>5</sub> C <sub>5</sub> C <sub>5</sub> C <sub>5</sub> U <sub>5</sub> U <sub>5</sub> A <sub>5</sub> A <sub>5</sub> C <sub>5</sub> U <sub>5</sub> C <sub>5</sub> A <sub>5</sub> G <sub>5</sub> T <sub>5</sub> T	305
29707	FLT1:2360L21 siNA (2340C) (antisense) stab2	U <sub>5</sub> U <sub>5</sub> G <sub>5</sub> U <sub>5</sub> U <sub>5</sub> G <sub>5</sub> U <sub>5</sub> A <sub>5</sub> U <sub>5</sub> U <sub>5</sub> G <sub>5</sub> U <sub>5</sub> G <sub>5</sub> U <sub>5</sub> G <sub>5</sub> T <sub>5</sub> T	306
29708	FLT1:3932L21 siNA (3912C) (antisense) stab2	G <sub>5</sub> G <sub>5</sub> U <sub>5</sub> U <sub>5</sub> U <sub>5</sub> G <sub>5</sub> A <sub>5</sub> U <sub>5</sub> C <sub>5</sub> U <sub>5</sub> C <sub>5</sub> A <sub>5</sub> G <sub>5</sub> T <sub>5</sub> T	307

Sirna/ RPI#	Aliases	Sequence	SEQ ID#
29709	FLT1:2969L21 siNA (2949C) (antisense) stab2	C <sub>5</sub> A <sub>5</sub> U <sub>5</sub> C <sub>5</sub> A <sub>5</sub> G <sub>5</sub> A <sub>5</sub> G <sub>5</sub> C <sub>5</sub> C <sub>5</sub> U <sub>5</sub> C <sub>5</sub> C <sub>5</sub> U <sub>5</sub> G <sub>5</sub> C <sub>5</sub> T <sub>5</sub> T	308
28030	Sirna/RPI GL2 Str1 (sense)	GGCAUUGGCCAACGUAACGCGGAAUACUUCGGAUUCGGUUAACGAA	309
28242	Sirna/RPI GL2 Str1 (sense) 2'-OMe	CGUACGCGGAAUACUUCGAUU	310
28243	Sirna/RPI GL2 Str1 (sense) 14 5' 2'-O-Me	CGUACGCGGAAUACUUCGATT	311
28244	Sirna/RPI GL2 Str1 (sense) 10 5' 2'-O-Me	CGUACGCGGAAUACUUCGATT	312
28245	Sirna/RPI GL2 Str1 (sense) 5 5' 2'-O-Me	CGUACGCGGAAUACUUCGATT	313
28246	Sirna/RPI GL2 Str2 (antisense) all 2'-O-me	UCGAAGUAUUCCGCGGUACGUU	314
28247	Sirna/RPI GL2 Str2 (antisense) all ribo pyrimidines = 2'-Ome	UCGAAGUAUUCCGCGGUACGUU	315
28248	Sirna/RPI GL2 Str2 (antisense) 5' 14 2'-O- Me	UCGAAGUAUUCCGCGGUACGTT	316
28249	Sirna/RPI GL2 Str2 (antisense) 5' 10 2'-O- Me	UCGAAGUAUUCCGCGGUACGTT	317
28250	Sirna/RPI GL2 Str2 (antisense) 5' 2'-O-Me	UCGAAGUAUUCCGCGGUACGTT	318
28251	Sirna/RPI GL2 Str1 (sense) all pyrimidines 2'-O-Me except 3'-TT	CGUACGCGGAAUACUUCGATT	319
28252	Sirna/RPI GL2 Str1 (sense) all pyrimidines = 2'-OMe	CGUACGCGGAAUACUUCGAUU	320
28253	Sirna/RPI GL2 Str1 (sense)+ TT =P=S	CGUACGCGGAAUACUUCGAT <sub>5</sub> T	321
28261	Sirna/RPI GL2 Str2 (antisense) all ribo pyrimidines = 2'-O-me, except 3'-TT	UCGAAGUAUUCCGCGGUACGTT	322
28257	Sirna/RPI GL2 Str1 (sense)+ 3' univ. base 2	CGUACGCGGAAUACUUCGAXX	323
28258	Sirna/RPI GL2 Str1 (sense)+ 3' univ base 1	CGUACGCGGAAUACUUCGAZZ	324
28259	Sirna/RPI GL2 Str2 (antisense), + 3' univ. base 2	UCGAAGUAUUCCGCGGUACGXX	325
28260	Sirna/RPI GL2 Str2 (antisense), + 3' univ. base 1	UCGAAGUAUUCCGCGGUACGZZ	326
28014	Sirna/RPI GL2 Str1 (sense) 5'ligation fragment P=Scapped Y-2'F	c <sub>5</sub> G <sub>5</sub> u <sub>5</sub> A <sub>5</sub> cG	327
28015	Sirna/RPI GL2 Str1 (sense) 3' ligation fragment P=Scapped Y-2'F	cGGAUAUAcuuc <sub>5</sub> C <sub>5</sub> A <sub>5</sub> T <sub>5</sub> T	328
28026	Sirna/RPI GL2 Str1 (sense)P=Scapped Y- 2'F	c <sub>5</sub> G <sub>5</sub> u <sub>5</sub> A <sub>5</sub> cGcGGAUAuAcuuc <sub>5</sub> G <sub>5</sub> A <sub>5</sub> T <sub>5</sub> T	329
28016	Sirna/RPI GL2 Str2 (antisense) 5' ligation	u <sub>5</sub> C <sub>5</sub> G <sub>5</sub> A <sub>5</sub> AGuA	330

Sirna/ RPI#	Aliases	Sequence	SEQ ID#
	fragment P=Scapped Y-2'F		
28017	Sirna/RPI GL2 Str2 (antisense) 3'ligation fragment P=Scapped Y-2'F	uuuccGCGuA <sub>S</sub> C <sub>S</sub> G <sub>S</sub> T <sub>S</sub> T	331
28027	Sirna/RPI GL2 Str2 (antisense) P=Scapped Y-2'F	u <sub>S</sub> C <sub>S</sub> G <sub>S</sub> A <sub>S</sub> AGuAuuccGCGuA <sub>S</sub> C <sub>S</sub> G <sub>S</sub> T <sub>S</sub> T	332
28018	Sirna/RPI GL2 Str1 (sense) 5'ligation fragment 5'P=S Y-2'F	sCGuAcG	333
28019	Sirna/RPI GL2 Str1 (sense) 3' ligation fragment 5'P=S Y-2'F	cGGAAuAcuucGATT	334
28028	Sirna/RPI GL2 Str1 (sense) 5'P=S Y-2'F	sCGuAcGCGGAAuAcuucGATT	335
28020	Sirna/RPI GL2 Str2 (antisense) 5' ligation fragment 5'P=S Y-2'F	sucGAAGuA	336
28021	Sirna/RPI GL2 Str2 (antisense) 3'ligation fragment 5'P=S Y-2'F	uuuccGCGuAcGTT	337
28029	Sirna/RPI GL2 Str2 (antisense) 5'P=S Y- 2'F	sucGAAGuAuuccGCGuAcGTT	338
28022	Sirna/RPI Inverted GL2 Str1 (sense) P=Scapped Y-2'F	A <sub>S</sub> G <sub>S</sub> C <sub>S</sub> u <sub>S</sub> ucAuAAAGGcGcAu <sub>S</sub> G <sub>S</sub> C <sub>S</sub> T <sub>S</sub> T	339
28023	Sirna/RPI Inverted GL2 Str2 (antisense) P=Scapped Y-2'F	G <sub>S</sub> C <sub>S</sub> A <sub>S</sub> u <sub>S</sub> GcGccuuAuGAAG <sub>S</sub> C <sub>S</sub> u <sub>S</sub> T <sub>S</sub> T	340
28024	Sirna/RPI Inverted GL2 Str1 (sense) 5'P=S Y-2'F	sAGcuucAuAAGGcGcAuGcTT	341
28025	Sirna/RPI Inverted GL2 Str2 (antisense) 5'P=S Y-2'F	sGcAuGcGccuuAuGAAGcuTT	342
28455	Sirna/RPI GL2 Str1 (sense) 2'-F U C	cGuAcGcGGAAuAcuucGATT	343
28456	Sirna/RPI GL2 Str2 (antisense) 2'-F U C	ucGAAGuAuuccGcGuAcGTT	344
29702	FLT1:349U21 siNA stab3 (sense)	c <sub>S</sub> u <sub>S</sub> G <sub>S</sub> A <sub>S</sub> GuuuAAAAGGcAc <sub>S</sub> C <sub>S</sub> T <sub>S</sub> T	345
29703	FLT1:2340U21 siNA stab3 (sense)	c <sub>S</sub> A <sub>S</sub> C <sub>S</sub> C <sub>S</sub> AcAAAAuAcAAc <sub>S</sub> A <sub>S</sub> T <sub>S</sub> T	346
29704	FLT1:3912U21 siNA stab3 (sense)	c <sub>S</sub> C <sub>S</sub> u <sub>S</sub> G <sub>S</sub> GAAAGAAucAAAA <sub>S</sub> C <sub>S</sub> T <sub>S</sub> T	347
29705	FLT1:2949U21 siNA stab3 (sense)	G <sub>S</sub> C <sub>S</sub> A <sub>S</sub> G <sub>S</sub> GGAGGGccucuGA <sub>S</sub> u <sub>S</sub> G <sub>S</sub> T <sub>S</sub> T	348
28443	Sirna/RPI GL2 Str1 (sense) 2'-amino U C	cGuAcGcGGAAuAcuucGATT	349
28444	Sirna/RPI GL2 Str2 (antisense) 2'-amino U C	ucGAAGuAuuccGcGuAcGTT	350
28445	Sirna/RPI GL2 Str1 (sense) 2'-amino U C UT 3'end	cGuAcGcGGAAuAcuucGAuT	351
28446	Sirna/RPI GL2 Str2 (antisense) 2'-amino U	ucGAAGuAuuccGcGuAcGuT	352

Sirna/ RPI#	Aliases	Sequence	SEQ ID#
	C uT 3'end		
30051	HCV-Luc:325U21 siNA 5' P=S + 3' univ. base 2 + 5'/3' invAba (antisense)	BC <sub>5</sub> C <sub>5</sub> C <sub>5</sub> C <sub>5</sub> G <sub>5</sub> GGAGGUCUCGUAGAXXB	353
30052	HCV-Luc:325U21 siNA rev 5' P=S + 3' univ. base 2 + 5'/3' invAba (antisense)	BA <sub>5</sub> G <sub>5</sub> A <sub>5</sub> U <sub>5</sub> G <sub>5</sub> CUCUGGAGGGCCCCCXXB	354
30053	HCV-Luc:345L21 siNA (325C) (antisense) 5' P=S + 3' univ. base 2 + 3' invAba (sense)	U <sub>5</sub> C <sub>5</sub> U <sub>5</sub> A <sub>5</sub> C <sub>5</sub> GAGACCUCGCCGGGGXXB	355
30054	HCV-Luc:345L21 siNA (325C) (antisense) rev 5' P=S + 3' univ. base 2 + 3' invAba (sense)	G <sub>5</sub> G <sub>5</sub> G <sub>5</sub> G <sub>5</sub> C <sub>5</sub> CCUCCAGAGCAUCUXXB	356
30055	HCV-Luc:325U21 siNA all Y P=S + 3' univ. base 2 + 5'/3' invAba (antisense)	BC <sub>5</sub> C <sub>5</sub> C <sub>5</sub> C <sub>5</sub> GGGAGGU <sub>5</sub> C <sub>5</sub> U <sub>5</sub> C <sub>5</sub> GU <sub>5</sub> AGAXXB	357
30056	HCV-Luc:325U21 siNA rev all Y P=S + 3' univ. base 2 + 5'/3' invAba (antisense)	BAGAU <sub>5</sub> GC <sub>5</sub> U <sub>5</sub> C <sub>5</sub> U <sub>5</sub> GGAGGGC <sub>5</sub> C <sub>5</sub> C <sub>5</sub> C <sub>5</sub> XXB	358
30057	HCV-Luc:345L21 siNA (325C) (antisense) all Y P=S + 3' univ. base 2 + 3' invAba (sense)	U <sub>5</sub> C <sub>5</sub> U <sub>5</sub> AC <sub>5</sub> GAGAC <sub>5</sub> C <sub>5</sub> U <sub>5</sub> C <sub>5</sub> C <sub>5</sub> C <sub>5</sub> GGGGXXB	359
30058	HCV-Luc:345L21 siNA (325C) (antisense) rev all Y P=S + 3' univ. base 2 + 3' invAba (sense)	GGGGC <sub>5</sub> C <sub>5</sub> C <sub>5</sub> U <sub>5</sub> C <sub>5</sub> C <sub>5</sub> AGAGC <sub>5</sub> AU <sub>5</sub> C <sub>5</sub> U <sub>5</sub> XXB	360
30059	HCV-Luc:325U21 siNA 4/3 P=S ends + all Y-2'F + 3' univ. base 2 + 5'/3' invAba (antisense)	Bc <sub>5</sub> C <sub>5</sub> S <sub>5</sub> C <sub>5</sub> GGGAGGucucGuA <sub>5</sub> G <sub>5</sub> A <sub>5</sub> XXB	361
30060	HCV-Luc:325U21 siNA rev 4/3 P=S ends + all Y-2'F + 3' univ. base 2 + 5'/3' invAba (antisense)	BA <sub>5</sub> G <sub>5</sub> A <sub>5</sub> u <sub>5</sub> GcucuGGAGGGcc <sub>5</sub> C <sub>5</sub> C <sub>5</sub> XXB	362
30170	HCV-Luc:325U21 siNA all Y-2'F + 3' univ. base 2 + 5'/3' invAba (antisense)	B cccccGGGAGGucucGuAGAXX B	363
30171	HCV-Luc:325U21 siNA rev all Y-2'F + 3' univ. base 2 + 5'/3' invAba (antisense)	B AGAuGcucuGGAGGGccccXX B	364
30172	HCV-Luc:345L21 siNA (325C) (antisense) all Y P=S + 3' univ. base 2 + 5'/3' invAba (antisense)	B U <sub>5</sub> C <sub>5</sub> U <sub>5</sub> AC <sub>5</sub> GAGAC <sub>5</sub> C <sub>5</sub> U <sub>5</sub> C <sub>5</sub> C <sub>5</sub> GGGGXX B	365
30173	HCV-Luc:345L21 siNA (325C) (antisense) all Y-2'F	ucuAcGAGAccucccGGGG	366
30174	HCV-Luc:345L21 siNA (325C) (antisense) rev all Y-2'F	GGGGccccuccAGAGcAucu	367



Sirna/ RPI#	Aliases	Sequence	SEQ ID#
30175	HCV-Luc:345L21 siNA (325C) (antisense) all Y-2'F + 3' univ. base 2	ucuAcGAGAccuccGGGGXX	368
30176	HCV-Luc:345L21 siNA (325C) (antisense) rev all Y-2'F + 3' univ. base 2	GGGGccuccAGAGcAucuXX	369
30177	HCV-Luc:345L21 siNA (325C) (antisense) all Y-2'F + 3' univ. base 2 + 5'3' iB	B ucuAcGAGAccuccGGGGXX B	370
30178	HCV-Luc:325U21 siNA all Y P=S + 3' univ. base 2 + 3' invAba (sense)	C <sub>5</sub> C <sub>5</sub> C <sub>5</sub> C <sub>5</sub> GGGAGGU <sub>5</sub> C <sub>5</sub> U <sub>5</sub> C <sub>5</sub> GU <sub>5</sub> AGAXX B	371
30063	Sirna/RPI GL2 Str1 (sense) 2'-F U,C + 3' ,5' abasic	BcGuAcGcGGAAuAucuGATTB	372
30222	Sirna/RPI GL2 Str1 (sense) Y 2'-O-Me with 3'-TT & 5'3' iB	B CGUACGCGGAAUACUUCGATT B	373
30224	Sirna/RPI GL2 Str2 (antisense) Y 2'-F & 3' TsT	ucGAAGuAuuccGcGuAcGT <sub>s</sub> T	374
30430	Sirna/RPI GL2 Str2 (antisense) 2'-F U,C + 5',3' abasic, A,G= 2'-O-Me	ucGAA <u>GuAuuccGcGuAcGT<sub>s</sub>T</u>	375
30431	Sirna/RPI GL2 Str1 (sense) 2'-F U,C + 3' ,5' abasic,TT; 2'-O-Me-A,G	BcGuAcGcGGAAuAucuGATTB	376
30433	Sirna/RPI GL2 Str1 (sense) 2'-F U,C + 3' ,5' abasic,TT; 2'-deoxy-A,G	BcGuAcGcGGAAuAucuGATTB	377
30550	Sirna/RPI GL2 Str2 (antisense) 2'-F U,C 3'- dT <sub>s</sub> T	ucGAA <u>GuAuuccGcGuAcGT<sub>s</sub>T</u>	378
30555	Sirna/RPI GL2 Str2 (antisense) 2'-F U,C 3'- glycerol.T	ucGAA <u>GuAuuccGcGuAcGTL</u>	379
30556	Sirna/RPI GL2 Str2 (antisense) 2'-F U,C 3'- glycerol,2T	ucGAA <u>GuAuuccGcGuAcGTL</u>	380
30226	rev Sirna/RPI GL2 Str1 (sense) Y 2'-O-Me with 3'-TT & 5'3' iB	B AGCUUCAUAAGGGCGCAUGCTT B	381
30227	rev Sirna/RPI GL2 Str1 (sense) Y 2'-F with 3'-TT & 5'3' iB	B AGcuuAuAAGGcGcAuGcTT B	382
30229	rev Sirna/RPI GL2 Str2 (antisense) Y 2'-F & 3' TsT	GcAuGcGccuuAuGAA <u>GcuT<sub>s</sub>T</u>	383
30434	Sirna/RPI GL2 Str1 (sense) 2'-F U,C + 3' ,5' Abasic,TT; 2'-O-Me-A,G;ribo core	BcGuAcGcGGAAuAucuGATTB	384
30435	Sirna/RPI GL2 Str1 (sense) 2'-F U,C + 3' ,5' Abasic,TT; 2'-deoxyA,G;ribo core	BcGuAcGcGGAAuAucuGATTB	385
30546	Sirna/RPI GL2 Str2 (antisense) 2'-F U,C 3'- dT <sub>s</sub> T	ucGAA <u>GuAuuccGcGuAcG3T</u>	386

SiRNA/ RPI#	Aliases	Sequence	SEQ ID#
30551	SiRNA/RPI GL2 Str2 (antisense) 2'-F U,C dTddC	ucGAAGuAuuccGcGuAcGTddC	387
30557	SiRNA/RPI GL2 Str2 (antisense) 2'-F U,C 3'- invertedT,T	ucGAAGuAuuccGcGuAcGT	388
30558	SiRNA/RPI GL2 Str2 (antisense) 2'-F U,C 3'- invertedT,TT	ucGAAGuAuuccGcGuAcGT T	389
30196	FLT1:2340U21 siRNA sense iB caps w/2'FY's	B cAAccAcAAAAuAcAAcAATT B	419
30416	FLT1:2358L21 siRNA (2340C) (antisense) Tst	uuGuuGuAuuuuGuGGuuGT <sub>s</sub> T	420
29548	HBV:394L21 siRNA (414C) (antisense)	GAUGAGGGCAUAGCAGCAGGTT	421
29544	HBV:414U21 siRNA pos (sense)	CCUGCUGCUAUGCCUCAUCTT	422
29556	HBV:394L21 siRNA neg (414C) (antisense) inv	GGACGACGAUACGGAGUAGTT	423
29552	HBV:414U21 siRNA pos (sense) inv	CUACUCCGUUUCGUGUCCTT	424
30350	HBV:262U21 siRNA stab04 (sense)	B uGGAcuucucucAAuuuuuA B	425
30361	HBV:280L21 siRNA (262C) (antisense) stab05	GAAAAuuGAGAGAAGuccAT <sub>s</sub> T	426
30372	HBV:262U21 siRNA inv stab04 (sense)	B AucuuuuAAcucucuuuAGGu B	427
30383	HBV:280L21 siRNA (262C) (antisense) inv stab05	AccuGAAGAGAGuuAAAAAGT <sub>s</sub> T	428
30352	HBV:380U21 siRNA stab04 (sense)	B uGuGuGuGcGGcGuuuuAucA B	429
30363	HBV:398L21 siRNA (380C) (antisense) stab05	AuAAAAcGccGcAGAcAcAT <sub>s</sub> T	430
30374	HBV:380U21 siRNA inv stab04 (sense)	B AcuAuuuuGcGGcGucGuGu B	431
30385	HBV:398L21 siRNA (380C) (antisense) inv stab05	AcAcAGAcGccGcAAAAuAT <sub>s</sub> T	432
30353	HBV:413U21 siRNA stab04 (sense)	B uccuGcuGcuAuGccucAucu B	433
30364	HBV:431L21 siRNA (413C) (antisense) stab05	AuGAGGcAuAGcAGcAGGAT <sub>s</sub> T	434
30375	HBV:413U21 siRNA inv stab04 (sense)	B ucuAcuccGuAucGucGuccu B	435
30386	HBV:431L21 siRNA (413C) (antisense) inv stab05	AGGAcGAcGAuAcGGAGuAT <sub>s</sub> T	436
30354	HBV:462U21 siRNA stab04 (sense)	B uAuGuuGcccGuuGuuccu B	437
30365	HBV:480L21 siRNA (462C) (antisense) stab05	AGGAcAAAcGGGcAAcAuAT <sub>s</sub> T	438

SiRNA/ RPI#	Aliases	Sequence	SEQ ID#
30376	HBV:462U21 siRNA inv stab04 (sense)	B ucuuccuuuuGcccGuuGuAu B	439
30387	HBV:480L21 siRNA (462C) (antisense) inv stab05	AuAcAAcGGGcAAAcAGGAT <sub>s</sub> T	440
30355	HBV:1580U21 siRNA stab04 (sense)	B uGuGcAcuucGcuucAccucu B	441
30366	HBV:1598L21 siRNA (1580C) (antisense) stab05	AGGuGAAgGcGAAAGuGcAcAT <sub>s</sub> T	442
30377	HBV:1580U21 siRNA inv stab04 (sense)	B ucuccAcuucGcuucAcGuGu B	443
30388	HBV:1598L21 siRNA (1580C) (antisense) inv stab05	AcAcGuGAAgGcGAAAGuGGAT <sub>s</sub> T	444
30356	HBV:1586U21 siRNA stab04 (sense)	B cuucGcuucAccucuGcAcGu B	445
30367	HBV:1604L21 siRNA (1586C) (antisense) stab05	GuGcAGAGGuGAAgGcGAAAGT <sub>s</sub> T	446
30378	HBV:1586U21 siRNA inv stab04 (sense)	B uGcAcGucuccAcuucGcuuc B	447
30389	HBV:1604L21 siRNA (1586C) (antisense) inv stab05	GAAgGcGAAAGuGGAGAcGuGT <sub>s</sub> T	448
30357	HBV:1780U21 siRNA stab04 (sense)	B AGGGuGuAGGcAuAAuGGGu B	449
30368	HBV:1798L21 siRNA (1780C) (antisense) stab05	cAAuuuAuGccuAcAGccuT <sub>s</sub> T	450
30379	HBV:1780U21 siRNA inv stab04 (sense)	B uGGuuAAuAcGGAuGucGGA B	451
30390	HBV:1798L21 siRNA (1780C) (antisense) inv stab05	uccGAcAuccGuAuuuAAcT <sub>s</sub> T	452
30612	HBV:1580U21 siRNA stab07 (sense)	B uGuGcAcuucGcuucAccuTT B	453
30620	HBV:1598L21 siRNA (1580C) (antisense) stab08	AGGuGAAgGcGAAAGuGcAcAT <sub>s</sub> T	454
30628	HBV:1582U21 siRNA inv stab07 (sense)	B ucuccAcuucGcuucAcGuTT B	455
30636	HBV:1596L21 siRNA (1578C) (antisense) inv stab08	GcAcAcGuGAAgGcGAAAGuGT <sub>s</sub> T	456
30612	HBV:1580U21 siRNA stab07 (sense)	B uGuGcAcuucGcuucAccuTT B	457
31175	HBV:1598L21 siRNA (1580C) stab11 (antisense)	AGGuGAAgGcGAAAGuGcAcAT <sub>s</sub> T	458
30612	HBV:1580U21 siRNA stab07 (sense)	B uGuGcAcuucGcuucAccuTT B	459
31176	HBV:1596L21 siRNA (1578C) (antisense) inv stab11 (antisense)	GcAcAcGuGAAgGcGAAAGuGT <sub>s</sub> T	460
30287	HBV:1580U21 siRNA (sense)	UGUGCACUUCGCUUCACCCUCU	461
30298	HBV:1598L21 siRNA (1580C) (antisense)	AGGUGAAgGcGAAAGUGCACACG	462
30355	HBV:1580U21 siRNA stab04 (sense)	B uGuGcAcuucGcuucAccucu B	463

Sirna/ RPI#	Aliases	Sequence	SEQ ID#
30366	HBV:1598L21 siRNA (1580C) (antisense) stab05	AGGUGAAGcGAAGuGcAcATsT	464
30612	HBV:1580U21 siRNA stab07 (sense) HBV:1598L21 siRNA (1580C) stab11 (antisense)	B uGuGcAcuucGcuucAccuTT B	465
31175		AGGUGAAGcGAAGuGcAcATsT	466
30612	HBV:1580U21 siRNA stab07 (sense) HBV:1598L21 siRNA (1580C) (antisense) stab08	B uGuGcAcuucGcuucAccuTT B	467
30620		AGGUGAAGcGAAGuGcAcATsT	468
31335	HBV:1580U21 siRNA stab09 (sense) HBV:1598L21 siRNA (1580C) stab10 (antisense)	B UGUGCACUUCGCUUCACCU TT B	469
31337		AGGUGAAGcGAAGUGCACATsT	470
31456	HCVa:291U21 siRNA stab04	B cuuGuGGuAcuGccuGAuATT B	471
31468	HCVa:309L21 siRNA (291C) stab05	uAucAGGcAGuAccAcAAGTsT	472
31480	HCVa:291U21 siRNA inv stab04	B AuAGuccGucAuGGGuGuuTT B	473
31492	HCVa:309L21 siRNA (291C) inv stab05	GAACcAuGAGcGGAcuAuTsT	474
31461	HCVa:300U21 siRNA stab04	B cuGccuGAuAGGGGuGcuuGTT B	475
31473	HCVa:318L21 siRNA (300C) stab05	cAAGcAccuAucAGGcAGTsT	476
31485	HCVa:300U21 siRNA inv stab04	B GuucGuGGGuAuAGuccGucTT B	477
31497	HCVa:318L21 siRNA (300C) inv stab05	GAcGGAcuAucccAcGAACtsT	478
31463	HCVa:303U21 siRNA stab04	B ccuGAuAGGGGuGcuuGcGATT B	479
31475	HCVa:321L21 siRNA (303C) stab05	ucGcAAGcAccuAucAGGTsT	480
31487	HCVa:303U21 siRNA inv stab04	B AGcGuucGuGGGuAuAGuccTT B	481
31499	HCVa:321L21 siRNA (303C) inv stab05	GGAcuAucccAcGAACGcuTsT	482
31344	HCVa:325U21 siRNA stab07	B ccccGGGAGGGuucGuAGATT B	483
30562	HCVa:345L21 siRNA (325C) Y-2'F, R- 2'OMe + TsT	ucuAcGAGAccucccGGGGTsT	484
31345	HCVa:325U21 siRNA inv stab07	B AGAuGcuucGGAGGGGccccTT B	485
31346	HCVa:343L21 siRNA (325C) inv stab08	GGGGccccuccAGAGcAucuTsT	486
31702	HCVa:326U21 siRNA stab07	B cccGGGAGGGuucGuAGAcTT B	487
31706	HCVa:344L21 siRNA (326C) stab08	GucuAcGAGAccucccGGGTsT	488
31710	HCVa:326U21 siRNA inv stab07	B cAGAuGcuucGGAGGGGccccTT B	489
31714	HCVa:344L21 siRNA (326C) inv stab08	GGGccccuccAGAGcAucuGTsT	490
31703	HCVa:327U21 siRNA stab07	B cccGGGAGGGuucGuAGAcTT B	491
31707	HCVa:345L21 siRNA (327C) stab08	GGGuuAcGAGAccucccGGTsT	492

SiRNA/ RPI#	Aliases	Sequence	SEQ ID#
31711	HCVa:327U21 siRNA inv stab07	B ccAGAuGcuuGGAGGGccTT B	493
31715	HCVa:345L21 siRNA (327C) inv stab08	GGccuccAGAGcAucuGGTtT	494
31704	HCVa:328U21 siRNA stab07	B cGGGAGGgucGuAGAccGTT B	495
31708	HCVa:346L21 siRNA (328C) stab08	cGGucAcGAGAccucccGTtT	496
31712	HCVa:328U21 siRNA inv stab07	B GccAGAuGcuuGGAGGGcTT B	497
31716	HCVa:346L21 siRNA (328C) inv stab08	GccuccAGAGcAucuGGcTtT	498
31705	HCVa:329U21 siRNA stab07	B GGGAGGgucGuAGAccGuTT B	499
31709	HCVa:347L21 siRNA (329C) stab08	AcGGucAcGAGAccucccTtT	500
31713	HCVa:329U21 siRNA inv stab07	B uGccAGAuGcuuGGAGGGTT B	501
31717	HCVa:347L21 siRNA (329C) inv stab08	ccuccAGAGcAucuGGcAtTt	502
31703	HCVa:327U21 siRNA stab07	B ccGGGAGGgucGuAGAccTT B	503
31707	HCVa:345L21 siRNA (327C) stab08	GGucAcGAGAccucccGGTtT	504
31711	HCVa:327U21 siRNA inv stab07	B ccAGAuGcuuGGAGGGccTT B	505
31715	HCVa:345L21 siRNA (327C) inv stab08	GGccuccAGAGcAucuGGTtT	506
29579	HCVa:325U21 siRNA	CCCCGGGAGGUCUCGUAGACCGU	543
	HCVa:327 siRNA 3'-classl 10bp	UCUCGUAGACCUUGGUCUACGAGACCUCGCCGTT	544
	HCVa:327 siRNA 3'-classl 8bp	UCGUAGACCUUGGUCUACGAGACCUCGCCGTT	545
	HCVa:327 siRNA 3'-classl 6bp	GUAGACCUUGGUCUACGAGACCUCGCCGTT	546
	HCVa:327 siRNA 3'-classl 4bp	AGACCUUGGUCUACGAGACCUCGCCGTT	547
	HCVa:327 siRNA 5'-classl 10bp	GGUCUACGAGACCUCGCCGUUCCGGGAGGUCU	548
	HCVa:327 siRNA 5'-classl 8bp	GGUCUACGAGACCUCGCCGUUCCGGGAGGU	549
	HCVa:327 siRNA 5'-classl 6bp	GGUCUACGAGACCUCGCCGUUCCGGGAG	550
	HCVa:327 siRNA 5'-classl 4bp	GGUCUACGAGACCUCGCCGUUCCGGG	551
	HCVa:327 siRNA 3'-gaaa 10bp	CUCGUAGACCGAAAGGUCUACGAGACCUCGCCGTT	552
	HCVa:327 siRNA 3'-gaaa 8bp	CGUAGACCGAAAGGUCUACGAGACCUCGCCGTT	553
	HCVa:327 siRNA 3'-gaaa 6bp	UAGACCGAAAGGUCUACGAGACCUCGCCGTT	554
	HCVa:327 siRNA 3'-gaaa 4bp	GACCGAAAGGUCUACGAGACCUCGCCGTT	555
	HCVa:327 siRNA 5'-gaaa 10bp	GGUCUACGAGACCUCGCCGUUGAAACCGGGAGGUC	556
	HCVa:327 siRNA 5'-gaaa 8bp	GGUCUACGAGACCUCGCCGUUGAAACCGGGAGG	557
	HCVa:327 siRNA 5'-gaaa 6bp	GGUCUACGAGACCUCGCCGUUGAAACCGGGA	558
	HCVa:327 siRNA 5'-gaaa 4bp	GGUCUACGAGACCUCGCCGUUGAAACCGG	559
	HCVa:327 siRNA 3'-uuuguguag 10bp	CGUAGACCUUUUGUAGGGUCUACGAGACCUCGCCGTT	560

Sirna/ RPI#	Aliases	Sequence	SEQ ID#
	HCVa:327 siRNA 3'-uuuguguag 8bp	UAGACCUUUUUUGUGUAGGGUCUACGAGACCUCCCGGTT	561
	HCVa:327 siRNA 3'-uuuguguag 6bp	GACCUUUUUUGUGUAGGGUCUACGAGACCUCCCGGTT	562
	HCVa:327 siRNA 3'-uuuguguag 4bp	CCUUUUUGUGUAGGGUCUACGAGACCUCCCGGTT	563
	HCVa:327 siRNA 5'-uuuguguag 10bp	GGUCUACGAGACCUCCCGGUUUUUUGUAGCGGGGAGGUC	564
	HCVa:327 siRNA 5'-uuuguguag 8bp	GGUCUACGAGACCUCCCGGUUUUUUGUAGCGGGAGG	565
	HCVa:327 siRNA 5'-uuuguguag 6bp	GGUCUACGAGACCUCCCGGUUUUUUGUAGCGGGGA	566
	HCVa:327 siRNA 5'-uuuguguag 4bp	GGUCUACGAGACCUCCCGGUUUUUUGUAGCGCGG	567
	HCVa:327 siRNA 3'-classl 10bp stab08	ucucGuAGAccuuGGucuAcGAGAccucccccGGTst	568
	HCVa:327 siRNA 3'-classl 8bp stab08	ucGuAGAccuuGGucuAcGAGAccucccccGGTst	569
	HCVa:327 siRNA 3'-classl 6bp stab08	GuAGAccuuGGucuAcGAGAccucccccGGTst	570
	HCVa:327 siRNA 3'-classl 4bp stab08	AGAccuuGGucuAcGAGAccucccccGGTst	571
	HCVa:327 siRNA 5'-classl 10bp stab08	GGucuAcGAGAccucccccGGuuccGGGAGGucu	572
	HCVa:327 siRNA 5'-classl 8bp stab08	GGucuAcGAGAccucccccGGuuccGGGAGGu	573
	HCVa:327 siRNA 5'-classl 6bp stab08	GGucuAcGAGAccucccccGGuuccGGGAG	574
	HCVa:327 siRNA 5'-classl 4bp stab08	GGucuAcGAGAccucccccGGuuccGGG	575
	HCVa:327 siRNA 3'-gaaa 10bp stab08	cucGuAGAccGAAAGGucuAcGAGAccucccccGGTst	576
	HCVa:327 siRNA 3'-gaaa 8bp stab08	cGuAGAccGAAAGGucuAcGAGAccucccccGGTst	577
	HCVa:327 siRNA 3'-gaaa 6bp stab08	uAGAccGAAAGGucuAcGAGAccucccccGGTst	578
	HCVa:327 siRNA 3'-gaaa 4bp stab08	GAccGAAAGGucuAcGAGAccucccccGGTst	579
	HCVa:327 siRNA 5'-gaaa 10bp stab08	GGucuAcGAGAccucccccGGuuGAAAccGGGAGGuc	580
	HCVa:327 siRNA 5'-gaaa 8bp stab08	GGucuAcGAGAccucccccGGuuGAAAccGGGAGG	581
	HCVa:327 siRNA 5'-gaaa 6bp stab08	GGucuAcGAGAccucccccGGuuGAAAccGGGA	582
	HCVa:327 siRNA 5'-gaaa 4bp stab08	GGucuAcGAGAccucccccGGuuGAAAccGG	583
	stab08	cGuAGAccuuuuuuGuGuAGGGGucuAcGAGAccucccccGGTst	584
	HCVa:327 siRNA 3'-uuuguguag 8bp	stab08	585
	HCVa:327 siRNA 3'-uuuguguag 6bp	stab08	586
	HCVa:327 siRNA 3'-uuuguguag 4bp	stab08	587
	HCVa:327 siRNA 5'-uuuguguag 10bp	stab08	588
	HCVa:327 siRNA 5'-uuuguguag 8bp	stab08	589

SiRNA/ RPI#	Aliases	Sequence	SEQ ID#
	stab08		
	HCVa:327 siRNA 5'-uuuguguag 6bp stab08		590
	HCVa:327 siRNA 5'-uuuguguag 4bp stab08	GGGucUAcGAGAccucccGGuuuuuGuGuAGccGGGA	591
	HCVa:347L23 siRNA (327C) stab08	GGGucUAcGAGAccucccGGuuuuuGuGuAGccGG	592
	HCVa:346L22 siRNA (327C) stab08	acGGGucUAcGAGAccucccGGTsT	593
	HCVa:345L21 siRNA (327C) stab08	cGGGucUAcGAGAccucccGGTsT	594
	HCVa:344L20 siRNA (327C) stab08	GGGucUAcGAGAccucccGGTsT	595
	HCVa:343L19 siRNA (327C) stab08	GucUAcGAGAccucccGGTsT	596
	HCVa:342L18 siRNA (327C) stab08	ucUAcGAGAccucccGGTsT	597
	HCVa:341L17 siRNA (327C) stab08	cuAcGAGAccucccGGTsT	598
	HCVa:340L16 siRNA (327C) stab08	uAcGAGAccucccGGTsT	599
	HCVa:339L15 siRNA (327C) stab08	AcGAGAccucccGGTsT	600
	HCVa:345L21 siRNA (327C) stab08 GG	cGAGAccucccGGTsT	601
	HCVa:345L20 siRNA (327C) stab08 G	GGGucUAcGAGAccucccGGsG	602
	HCVa:345L20 siRNA (327C) stab08	GGGucUAcGAGAccucccGGsG	603
	HCVa:345L19 siRNA (327C) stab08	GGGucUAcGAGAccucccGGsT	604
	HCVa:345L18 siRNA (327C) stab08	GGGucUAcGAGAccucccGsG	605
	HCVa:345L17 siRNA (327C) stab08	GGGucUAcGAGAccuccsG	606
	HCVa:345L16 siRNA (327C) stab08	GGGucUAcGAGAccuccsc	607
	HCVa:345L15 siRNA (327C) stab08	GGGucUAcGAGAccusc	608
	HCVa:327U21 siRNA stab07	B ccGGGAGGucucGuAGaccTT B	609
	HCVa:327U21 siRNA stab07 GT	B ccGGGAGGucucGuAGaccGT B	610
	HCVa:327U21 siRNA stab07	B cGGGAGGucucGuAGaccTT B	611
	HCVa:328U20 siRNA stab07	B GGGAGGucucGuAGaccTT B	612
	HCVa:329U19 siRNA stab07	B GGAGGucucGuAGaccTT B	613
	HCVa:330U18 siRNA stab07	B GAGGucucGuAGaccTT B	614
	HCVa:331U17 siRNA stab07	B AGGucucGuAGaccTT B	615
	HCVa:332U16 siRNA stab07	B ccGGGAGGucucGuAGaccT B	616
	HCVa:327U21 siRNA stab07	B ccGGGAGGucucGuAGacc B	617
	HCVa:327U21 siRNA stab07	B ccGGGAGGucucGuAGac B	618

SiRNA/ RPI#	Aliases	Sequence	SEQ ID#
	HCVa:327U21 siRNA stab07	B ccGGGAGGucucGuAGA B	619
	HCVa:327U21 siRNA stab07	B ccGGGAGGucucGuAG B	620
31270	FLT1:349U21 siRNA stab09 sense	B CUGAGUUUAAAAGGCACCCCTT B	621
31273	FLT1:367L21 siRNA (349C) stab10 antisense	GGGUGCCUUUUAAACUCAGTsT	622
31276	FLT1:349U21 siRNA stab09 inv sense	B CCCACGGAAAAUUUGAGUCITT B	623
31279	FLT1:367L21 siRNA (349C) stab10 inv antisense	GACUCAAUUUUCCGUGGGTsT	624
31679	HBV:1598 all RNA sense	AGGUGAAGCGAAGUGCACAUU	625
30287	HBV:1598 all RNA antisense	UGUGCACUUUCGUUCACCCUCU	626
31336	HBV:1580U21 siRNA inv stab09 sense	B UCCACUUCGCUUCACGUGUTT B	627
31338	HBV:1598L21 siRNA (1580C) inv stab10 antisense	ACACGUGAAGCGAAGUGGATsT	629
32636	Luc3:80U21 siRNA stab07 sense	B AuAAGGcuAuGAAGAGAuATT B	630
32676	Luc3:98L21 siRNA (80C) stab08 antisense	uAucucuuAuAGccuuAuTsT	631
32640	Luc3:237U21 siRNA stab07 sense	B cGuAuGcAGUGAAAAAcucUTT B	632
32680	Luc3:255L21 siRNA (237C) stab08 antisense	AGAGuuuuAcuGcAuAcGTsT	633
32662	Luc3:1478U21 siRNA stab07 sense	B uGAcGGAAAAAGAGAcuGUTT B	634
32702	Luc3:1496L21 siRNA (1478C) stab08 antisense	AcGAucucuuuuuccGucATsT	635
32666	Luc3:1544U21 siRNA stab07 sense	B GAGuuGuGuuuGuGGAcGATT B	636
32706	Luc3:1562L21 siRNA (1544C) stab08 antisense	ucGuccAcAAAcAcAcucTsT	637
32672	Luc3:1607U21 siRNA stab07 sense	B GAGAGAuuccucAuAAAGGcTT B	638
32712	Luc3:1625L21 siRNA (1607C) stab08 antisense	GccuuuAuGAGGAucucucTsT	639
33139	HCVa:282U21 siRNA stab07 sense	B GcGAAAGGccuuGuGGuAcTT B	640
33179	HCVa:300L21 siRNA (282C) stab08 antisense	GuAccAcAAGGccuuuuccGcTsT	641
33140	HCVa:283U21 siRNA stab07 sense	B cGAAAGGccuuGuGGuAcuTT B	642
33180	HCVa:301L21 siRNA (283C) stab08 antisense	AGuAccAcAAGGccuuuuccGTsT	643
33145	HCVa:289U21 siRNA stab07 sense	B GccuuGuGGuAuGccuGATT B	644
33185	HCVa:307L21 siRNA (289C) stab08 antisense	ucAGGcAGuAccAcAAGGcTsT	645



SiRNA/ RPI#	Aliases	Sequence	SEQ ID#
	antisense		
33149	HCVa:304U21 siRNA stab07 sense HCVa:304L21 siRNA (286C) stab08	B cuGAuAGGGGuGcuuGcGAGTT B	646
33183	antisense	GGcAGuAccAcAAGGccuuTsT	647
33150	HCVa:305U21 siRNA stab07 sense HCVa:323L21 siRNA (305C) stab08	B uGAuAGGGGuGcuuGcGAGuTT B	648
33190	antisense	AcucGcAAAGcAcccuAucATsT	649
33151	HCVa:307U21 siRNA stab07 sense HCVa:325L21 siRNA (307C) stab08	B AuAGGGGuGcuuGcGAGuGcTT B	650
33191	antisense	GcAcucGcAAAGcAcccuAuTsT	651
33158	HCVa:317U21 siRNA stab07 sense HCVa:317L21 siRNA (299C) stab08	B uGcGAGuGccccGGGAGuTT B	652
33187	antisense	AAGcAcccuAucAGGcAGuTsT	653
33210	HBV:258U21 siRNA stab07 sense HBV:276L21 siRNA (258C) stab08	B GuGGuGGAcuucucucAAuTT B	654
33250	antisense	AuuGAGAGAAAGuccAccAcTsT	655
33212	HBV:260U21 siRNA stab07 sense HBV:278L21 siRNA (260C) stab08	B GGGuGGAcuucucucAAuuuTT B	656
33252	antisense	AAuuuGAGAGAAAGuccAccTsT	657
33214	HBV:263U21 siRNA stab07 sense HBV:281L21 siRNA (263C) stab08	B GGAcuucucucAAuuuucTT B	658
33254	antisense	AGAAAAuuGAGAGAAAGuccTsT	659
32429	HBV:1583U21 siRNA stab07 sense HBV:1601L21 siRNA (1583C) stab08	B GcAcuucGcuucAcccuGTT B	660
32438	antisense	cAGAGGuGAAGcGAAGuGcTsT	661
33226	HBV:1585U21 siRNA stab07 sense HBV:1603L21 siRNA (1585C) stab08	B AcuucGcuucAcccuGcATT B	662
33266	antisense	uGcAGAGGuGAAGcGAAGuTsT	663
31651	HBV:1580U21 siRNA stab06 sense	B UGUGCACUUCGCUUCACCUUTT B	664
31652	HBV:1580U21 siRNA inv stab06 sense	B UCCACUUCGCUUCACGUGUUTT B	665
31653	HBV:1580U21 siRNA stab16 sense	B UGUGCACUUCGCUUCACCUUTT B	666
31654	HBV:1580U21 siRNA inv stab16 sense	B UCCACUUCGCUUCACGUGUUTT B	667
31657	HBV:1580U21 siRNA stab18 sense	B uGuGcAcuucGcuucAccuTT B	668
31658	HBV:1580U21 siRNA inv stab18 sense	B uccAcuucGcuucAccGuGuTT B	669

UPPER CASE = ribonucleotide  
UPPER CASE UNDERLINE = 2'-O-methyl nucleotide  
Lower case underline = 2'-deoxy-2'-amino nucleotide  
 Lower case = 2'-deoxy-2'-fluoro nucleotide  
 T = thymidine  
*T* = inverted thymidine  
 t = 3'-deoxy thymidine  
B = inverted deoxybasic succinate linker  
B = inverted deoxybasic  
 X = universal base (5-nitroindole)  
 Z = universal base (3-nitropyrrole)  
 S = phosphorothioate internucleotide linkage  
 U = 5-bromodeoxyuridine  
 A = deoxyadenosine  
 G = deoxyguanosine  
 L = glyceryl moiety  
 ddC = dideoxy Cytidine  
 p=phosphate